

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:48 ; Search time 2788.18 Seconds
(without alignments)
11304.265 Million cell updates/sec

Title: US-09-807-933B-6
Perfect score: 1083
Sequence: 1 atgaagctccttaccattgc.....ctggcgtctcaagaataa 1083

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pt:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pln:*
35: em_hg_rtd:*
36: em_hg_mam:*
37: em_hg_vrt:*
38: em_ey:*
39: em_hggo_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225.4	20.8	808	3 AB045178	AB045178 Reticulit
2	224.8	20.8	840	3 AB045172	AB045172 Reticulit
3	218.2	20.1	1443	8 FSOACH	AB045172 Reticulit
4	218.2	20.1	1473	6 A21795	AB045172 Reticulit
5	218.2	20.1	1473	6 A23637	AB045172 Reticulit
6	218.2	20.1	1473	6 A23646	AB045172 Reticulit
7	218.2	20.1	1473	6 A23955	AB045172 Reticulit
8	218.2	20.1	1473	6 A23959	AB045172 Reticulit
9	218.2	20.1	1473	6 A41660	AB045172 Reticulit
10	218.2	20.1	1473	6 AR072922	AB045172 Reticulit
11	218.2	20.1	1473	6 BD002249	AB045172 Reticulit
12	218.2	20.1	1473	6 BD010853	AB045172 Reticulit
13	218.2	20.1	1473	6 I13885	AB045172 Reticulit
14	218.2	20.1	1473	6 I21317	AB045172 Reticulit
15	218.2	20.1	1473	6 I57984	AB045172 Reticulit
16	214.4	19.8	784	3 AB045167	AB045167 Reticulit
17	213.8	19.7	781	3 AB045165	AB045165 Reticulit
18	212.8	19.6	780	3 AB045168	AB045168 Reticulit
19	212.8	19.6	785	3 AB045169	AB045169 Reticulit
20	208.8	19.3	774	3 AB045170	AB045170 Reticulit
21	208.8	19.3	828	3 AB045171	AB045171 Reticulit
22	206.4	19.1	710	3 AB045171	AB045171 Reticulit
23	205.4	19.0	1423	6 AR094309	AB045171 Reticulit
24	198.4	18.3	783	3 AB045173	AB045173 Reticulit
25	198.2	18.3	761	3 AB045175	AB045175 Reticulit
26	195	18.0	924	6 A68074	AB045175 Reticulit
27	195	18.0	924	6 A68074	AB045175 Reticulit
28	192	17.7	798	3 AB045166	AB045166 Reticulit
29	187.2	17.3	785	3 AB045177	AB045177 Reticulit
30	187.2	17.3	802	3 AB045176	AB045176 Reticulit
31	185.6	17.1	759	3 AB045174	AB045174 Reticulit
32	184.4	17.0	919	6 A68072	AB045174 Reticulit
33	184.4	17.0	919	6 A68072	AB045174 Reticulit
34	184.4	17.0	922	6 A68070	AB045174 Reticulit
35	184.4	17.0	922	6 A68070	AB045174 Reticulit
36	181	16.7	1174	6 A92311	AB045174 Reticulit
37	181	16.7	1174	6 A92311	AB045174 Reticulit
38	181	16.7	1174	6 A92311	AB045174 Reticulit
39	178.2	16.5	927	6 AR094307	AB045174 Reticulit
40	178	16.4	960	6 AR094305	AB045174 Reticulit
41	177	16.3	894	6 AR094306	AB045174 Reticulit
42	170.2	15.7	913	6 AR094311	AB045174 Reticulit
43	168.4	15.5	885	6 AR094316	AB045174 Reticulit
44	161.8	14.9	1057	6 BD002248	AB045174 Reticulit
45	161.8	14.9	1060	6 A21793	AB045174 Reticulit

ALIGNMENTS

RESULT 1
AB045178
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

AB045178 808 bp mRNA linear INV 14-FEB-2001
Reticulitermes speratus hindgut symbiont 130484 CDNA to mRNA,
cellulase homologue, clone:45-6, complete cds.
AB045178
AB045178.1 GI:8926988
Reticulitermes speratus hindgut symbiont 130484 CDNA to mRNA,
clone:45-6,
Unclassified.
REFERENCE
Ohkoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
Diverse genes of cellulase homologues of glycosyl hydrolase family

Db	310	GGAGGCGAAACGGGTCGTGTTGGCAATTGCTATGAGCTTACCTTCACAGTGGCCAGTT	369
Qy	754	AAGGTTAAGAAAGTGTGTTTCAAGTAACAACACTGTGTTGACCTTGGCTTAACT	813
Db	370	AATGAAAGAAAGTGTGTTTCAAGTTACGAACACCGGTGTGATCTTGGTTCAA	425
Qy	814	GGTGTCACCTTGACTTGCAATGACCCGGTGTGTGTGTGTGTATCTAATGTTGTGCC	873
Db	426	-----TCAATTGATCTTGCATTTCCCGAGAGAGTGTGGAAATTTACATGATGACT	480
Qy	874	ACTCAATGGGTGTCTCCACCGATGTGTGGGTGTGCAATACAGCGGTGTTCTTGTGCC	933
Db	481	CAACATACAGGGGGCCCTCCGATGATGAGGGAAGCCGATATGGTGTGTTCACTTGA	540
Qy	934	TCTGACTGTTTAACTTCTCTTGTGCGCTTCAAGCTGTGTGAATGAGATTGGCTGG	993
Db	541	TCTGAATGTTCTCAGCTTCATCAGTGTCTTCAAGCTGTGATCCAGTGAATTGATTGG	600
Qy	994	TTCAAAAACGCTGATACCCCAACATGACCTACAAAGTTACTCTGCCAAGCTATC	1053
Db	601	TTCCAAAATGCTGACCAACCTTCAATCAATTCAATCAAGTACCTGCCAAGTATGG	660
Qy	1054	ACTCCCAAGTCTGGCTGTTCAAGAAATTA	1083
Db	661	ACAGCAAAACCAATTCGACAGCACTTAA	690
RESULT 3			
FSOCH			
LOCUS	FSOCH	1443 bp	mRNA
DEFINITION	Fusarium oxysporum K-family cellulase homologue mRNA, complete cds.		
ACCESSION	L29381		
VERSION	L29381.1	GI:520822	
KEYWORDS	K-family cellulase homologue; cellulase; homologue.		
SOURCE	Fusarium oxysporum CDNA to mRNA.		
ORGANISM	Fusarium oxysporum		
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.		
REFERENCE	1. (bases 1 to 1443)		
AUTHORS	Sheppard, P.O., Grant, F.J., Oort, P.J., Sprenger, C.A., Foster, D.C., Hagen, F.S., Ushall, A., McNight, G.L. and O'Hara, P.J.		
TITLE	The use of conserved cellulase family-specific sequences to clone cellulase homologue cDNAs from Fusarium oxysporum		
JOURNAL	Gene 150 (1), 163-167 (1994)		
MEDLINE	95047531		
PUBMED	7959045		
FEATURES			
Source	Location/Qualifiers		
	1..1443		
	/organism="Fusarium oxysporum"		
	/db_xref="taxon:5507"		
	83..1213		
	/note="putative"		
	/codon_start=1		
	/product="K-family cellulase homologue"		
	/protein_id="AAA65589.1"		
	/db_xref="GI:520823"		
	/translation="MRSYTLALAGPLAVSAAGSGHSIRYDCKKPSGMSGAANVAAPALTDKNDNPISNTNVAVNCCEGGSAVACTYSPVAVNDLRYGPAATYISGSEFALGCACTALTTTGTGKVKKATVOSTTNRGDLGDHFDLAMPGGVGLFDGCTSEFGKALGCAQYGGISRSBECDSYBELKDGCHRWGPDWENADNPOTFEQVQCPVALDLSGCKRDDSSFPAPFKDPTASAKSPSSASAKTSAAALAPORTKSAIPVQKSTKPAKAPQEPETKPADKPTDTPKATKPAQPNVKKPTTQCRGTGTRGSCPAKTDAAKKAKKSVVPAVYCGGSKSAVPMGNLAATGSCVMQNEYYSQCVN"		
BASE COUNT	325 a	448 c	332 g
ORIGIN			338 t
Query Match	20.1%	Score 218.2;	DB 8; Length 1443;
Best Local Similarity	63.0%;	Pred. No. 1e-48;	
Matches 394;	Conservative	0; Mismatches 213;	Indels 18; Gaps 3;
Qy	449	GTGTCGCTCCGGTAAAGTGAACCACTTCGCTACTGGGATTTGTGAAGCTTTTGGCA	508

Db	129	GTGCTGCTTTCGGAAGGGGCTCACTCTACGTGATCTAGTGGATATGCTGCAAGGCTTCTTGGT	188
Oy	509	GTTGGCCCGGTAAGGCTGATGTCACTCTCCCTCTTGGGCTCTCTGTAAACAAGATGTAAGA	568
Db	189	CTTGGACCGGAAGGCTGTCTCAACCCCTCTTAACTTGTGATTAAGAACACAACC	248
Oy	569	CTTTGTGCGATTAACAACACTCAAAAGGAGCTGT---GTTGGTGTAGGACAGCTACACTGT	625
Db	249	CCATTTCCAAACCAACATGCTGTCAACGATTTGTAGGGGTGTGTGTTTCTTATGCTTGA	308
Oy	626	ATGCAATCAACCTTGGGTTGTTAGCGACGACCTTGCCTACGATTTTGCCGCTCTTCA	685
Db	309	CCAATCTCTCCCTGGGGCTGTCAACGATGAGCTTGGCTTACGGTTTGGCTGTACAAGA	368
Oy	686	TTTCTGTGTGTAGCGAAGCTACTTGTGTGTGTGTGCTTTCGAATCACTAACCTTCTA	745
Db	369	TCTCCGGGTGCTCCGAGGCGAGCTGTGTGTGTGTCTTATGCTTTGACCTTCACTCACTG	428
Oy	746	CTGCGCTTCAAGGGTAAAGATGTTTTCAGTAAGTAACAACACTGTGTTTGAACCTTGGCT	805
Db	429	GCCCCGTCAAGGGGAAGAAATGATGTGTCACTGTCACACCACTAGGAGGATATCTCGCG	488
Oy	806	CTAACACTGTGCTCACTTTGACTTTGCAAAATGCCCGGTGTGTGTGTGTATCTACAATG	865
Db	489	ACAAAC-----CACTTGATCTTCATGATGCGCGCGGTGTGTGTGTGTATCTTTCAGC	539
Oy	866	GTTGTGCACTCAATGAGGGGTCTCCCAACGATGTTGGGTGCAAGATACGCGGCTGTT	925
Db	540	GCTGCACCTCTGAGTTTCGG-----CAAGGCTCTCGGCGGGTCCAGTAACGCGGATCT	593
Oy	926	CTTCTGCTCTGACTGTTCCTTCACTTCTTCTTCTGCTTCAAGCTGTGTGTATGAGGAT	985
Db	594	CTTCCCGAAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	653
Oy	986	TCGGCTGGTTCAAAAACGCTGATTAACCAACCATGATCTTACAAACAAGTTACTGTCCCA	1045
Db	654	TCGACTGTTTGAAGAACCGGACCAACCTGACTTCACTTTGAGCAGGTTTCAAGTCCCA	713
Oy	1046	AGGCTATCTACTGCCAAGTCTGGCTG 1070	
Db	714	AGGCTCTCTCGACATCATGATGATG 738	

RESULT 4

A21795

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

1473 bp

mRNA

linear

PAT 20-SEP-1995

A21795

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

1473 bp

mRNA

linear

PAT 20-SEP-1995

FEATURES

source

CDS

Location/Qualifiers

1..1473

/organism="Fusarium oxysporum"

/strain="DSM 2672"

/db_xref="taxon:5507"

97..1227

/codon_start=1

/product="endonuclease"

/protein_id="CAO1575.1"

/db_xref="GI:1246875"

/translation="MRSYTLALAGPLAVSAAGSGHSTRVMDCKPSGWSGKRAVNV
APALCTKNDNPISNTNVAVNGCEGGSAVACTNTSPVAVDELAVGPAATRTSGSEB
SWCACVATPTTTPVPGKMI VOSTYTGDLGNHFDLMMPGGAVGIFDCSTGFG
ALGGAQVGGIISRSBCDSYPELLKDGCHMRPDMENDNDPFTFEVQCPVALDLSG
CKRDDSPAPFKVDTASAKRQPSSSAKTKTSAALAAQSPAVQKSTKPAAP
QPEPTKADKPDNDKPVATKPAATKPKVOPVNVKPTTQKVGKTKRSGCPAKTDATAKK
SVVPAIYQCGGSKAPYENGNLAKTSGKVNQNYRYSQCPVN"

BASE COUNT

343 a 453 c 337 g 340 t

ORIGIN

Query Match 20.1%; Score 218.2; DB 6; Length 1473;
 Best Local Similarity 63.0%; Pred. No. 1e-48;
 Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

449 GTGGTCCCTCCGGTAATGTTGAACCACTCGTACTGGGATGTTGTAAGCTTTCTTCA 508
 143 GTGCTGCTTCTGGAAGGGGTCACTACTGATCGATGCGATGTCGCAAGCTTCTTCT 202
 509 GTTGGCCCGTAAGAGTGTATGATCCTCCCTGTTGCTCTGTAACAGATGTAAGA 568
 203 CTGGAGCGGAAGGCTGTGTCAAGCCCTGCTTTAATTGATGATGAAAGCAACC 262
 569 CTCTGCTGATTAACAACACTCAAAAGGCTG---GTTGGTGTAGACGCTACCTGTA 625
 263 CCATTTCACACCAATGCTGTCAACGGTTGAGAGGTGGTGGTCTGCTTATGCTTCA 322
 626 ATGACATCAACCTTGGTGTGTAAGCAAGACTTGGCTAGCGTTTCCCGCTGCTTCA 685
 323 CCAACTACTCTCCCTGGGCTGTCAACGATGAGCTTGGCTAGCGTTTCCCGCTTCA 382
 686 TTTCTGCTGTAGGGAAGCTACTGTTGTTGCTGTTGCTGTAACCTACACTCTTA 745
 383 TCTCGGTGGCTCCGAGGCGAGCTGTGCTGTGCTGTTGCTGTAACCTTCAACTG 442
 746 CTGCGCTCAAGGTAAGATGTTGTTCAAGTAACCAACACTGTTCTGACTTGTGCT 805
 443 GCCCGCTCAAGGGAAGATGATGTCACACTGCAACCACTGAGGTTGATCTGCGCG 502
 806 CTAACTAGTGTCTCACTTGTGCAATGCCGAGTGTGGTGTGTTGATCTCAATG 865
 503 ACAAC-----CACTGATCTGATGATCCCGAGGAGTGTGGTGTGATCTTCAAG 553
 866 GTTGTGCCACTCAATGGGGTGTCTCCACCGATGTTGGGGTGAATAGCGGCTGTT 925
 554 GCTGACCTCTGAGTGG-----CAAGGCTCTGGGCGGCGGCAATAGCGGCTGATCT 607
 926 CTTCGCTCTGAGCTGTTCACTTCTTCTGCTTCCGCTTCAAGCTGTTGTAAGTGAAT 985
 608 CTCCCGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
 986 TGGGCTGTTCAAAAAGCTGATTAACCAACATGATGATGATGATGATGATGATGAT 1045
 668 TGAAGTGTGGAAGGCGGACCACTGATCTTCACTTGAAGAGTTCAAGTCCCA 727
 1046 AGGCTATCACTGCAAGTCTGCTG 1070
 728 AGGCTCTCTCGACATCAAGTGAATG 752

RESULT 5
 A23637 1473 bp mRNA linear PAT 1b-SEP-1995
 LOCUS F. oxysporum endoglucanase gene.
 DEFINITION A23637.1 GI:832888
 ACCESSION endoglucanase.
 VERSION
 KEYWORDS Fusarium oxysporum.
 SOURCE
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; microsporitic Hypocreales; Fusarium; Fusarium oxysporum
 complex; 1 (bases 1 to 1473)

REFERENCE
 AUTHORS Convents,A.C., Busch,A. and Baeck,A.C.
 TITLE Deletergent compositions with high activity cellulase and softening
 JOURNAL Patent: EP 0495258-A 3 22-JUL-1992;
 FEATURES
 SOURCE The PROCTER & GAMBLE COMPANY
 Location/Qualifiers
 1..1473
 /organism="Fusarium oxysporum"
 /db_xref="taxon:5507"

CDS

97..1227
 /codon_start=1
 /product="endoglucanase"
 /protein_id="CAA01682.1"
 /db_xref="GI:832889"
 /translation="MRSYTLTLLAAGPLVAASAGSGHSTRYDCKRPSGMSGAIVN
 APLATCDKNDNPI SMTNVAVNCBGGSAVAACNYSPPMVAINDLAVGFAARKISGSEA
 SWCCACVALFTPTGVPKGMIVOSTNTGDDGLDHPMLMPPGGVGIPGCTSRGK
 ALGAAQYGGISRSRSECDSEYPELLMDGCHNRPFMFNANPDFTPEYQCPKALDLSG
 CKDDSSSPAPKVDTSASKEPSSAKKTSAAAPQKTKDSAPVVKSTKPA
 QPEPTKAPKQPTDKVPATKPAATKPVQGVNPKTKTOKRVKTRGSCPAKTDATKA
 SVPAYVOCGSGSKSAVPNGNLACATSKSKVKNERYSCVEN"

BASE COUNT 343 a 453 c 337 g 340 t
 ORIGIN

Query Match 20.1%; Score 218.2; DB 6; Length 1473;
 Best Local Similarity 63.0%; Pred. No. 1e-48;
 Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

449 GTGGTCCCTCCGGTAATGTTGAACCACTCGTACTGGGATGTTGTAAGCTTTCTTCA 508
 143 GTGCTGCTTCTGGAAGGGGTCACTACTGATCGATGCGATGTCGCAAGCTTCTTCT 202
 509 GTTGGCCCGTAAGAGTGTATGATCCTCCCTGTTGCTCTGTAACAGATGTAAGA 568
 203 CTGGAGCGGAAGGCTGTGTCAAGCCCTGCTTTAATTGATGATGAAAGCAACC 262
 569 CTCTGCTGATTAACAACACTCAAAAGGCTG---GTTGGTGTAGACGCTACCTGTA 625
 263 CCATTTCACACCAATGCTGTCAACGGTTGAGAGGTGGTGGTCTGCTTATGCTTCA 322
 626 ATGACATCAACCTTGGTGTGTAAGCAAGACTTGGCTAGCGTTTCCCGCTGCTTCA 685
 323 CCAACTACTCTCCCTGGGCTGTCAACGATGAGCTTGGCTGCTGCTTCAACTG 382
 686 TTTCTGCTGTAGGGAAGCTACTGTTGTTGCTGTTTCAAGTCACTGACTTGTGCT 745
 383 TCTCGGTGGCTCCGAGGCGAGCTGTGCTGTGCTGTTGCTGTAACCTTCAACTG 442
 746 CTGCGCTCAAGGTAAGATGTTGTTCAAGTAACCAACCTGTTCTGACTTGTGCT 805
 443 GCCCGCTCAAGGGAAGATGATGTCACACTGCAACCACTGAGGTTGATCTGCGCG 502
 806 CTAACTAGTGTCTCACTTGTGCAATGCCGAGTGTGGTGTGTTGATCTCAATG 865
 503 ACAAC-----CACTGATCTGATGATCCCGAGGAGTGTGGTGTGATCTTCAAG 553
 866 GTTGTGCCACTCAATGGGGTGTCTCCACCGATGTTGGGGTGAATAGCGGCTGTT 925
 554 GCTGACCTCTGAGTGG-----CAAGGCTCTGGGCGGCGGCAATAGCGGCTGATCT 607
 926 CTTCGCTCTGAGCTGTTCACTTCTTCTGCTTCCGCTTCAAGCTGTTGTAAGTGAAT 985
 608 CTCCCGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
 986 TGGGCTGTTCAAAAAGCTGATTAACCAACATGATGATGATGATGATGATGATGAT 1045
 668 TGAAGTGTGGAAGGCGGACCACTGATCTTCACTTGAAGAGTTCAAGTCCCA 727
 1046 AGGCTATCACTGCAAGTCTGCTG 1070
 728 AGGCTCTCTCGACATCAAGTGAATG 752

RESULT 6
 A23646 1473 bp mRNA linear PAT 23-FEB-1995
 LOCUS F. oxysporum endoglucanase gene.
 DEFINITION A23646
 ACCESSION A23646.1 GI:832892
 VERSION
 KEYWORDS Fusarium oxysporum.
 SOURCE Fusarium oxysporum
 ORGANISM

QY 866 GTTGTGCACTGATGGGGTGTCTCCACGATGTTGGGATGCAAGATACGGCGGTGTT 925
 DB 554 GCTGCACTCTGATGTCG-----CAAGCTCTGGGGGCGCCAGTACGGCGGTATCT 607
 QY 926 CTCTGCTGCTGATGTTTAACTCTTCTTCTGCTTCTTCAAGCTGTTGTAAGGAGAT 985
 DB 608 CTTCCGGAAGCGAATGTGATGATACCTCCGAGCTTCTCAAGAGCGTTGCCACTGGGAT 667
 QY 986 TCGGCTGTTCAAAACGCTGATTAACCAACATGACCTACAAACAGTTACTGTCCA 1045
 DB 668 TCGACTGTTGCAAGCGCGACACCTGATCTTCACTTTAGCAGGTTCAGTGGCCCA 727
 QY 1046 AGGCTATCACTGCCAAGTCTGCTG 1070
 DB 728 AGGCTCTCTCGACATCAGTGATG 752

RESULT 8
 A23959 1473 bp DNA linear PAT 01-MAR-1995
 LOCUS Endoglucanase gene.
 DEFINITION A23959
 ACCESSION A23959 GI:832900
 VERSION A23959.1 GI:832900
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; Mitosporic Hypocreales; Fusarium; Fusarium oxysporum
 complex.

REFERENCE 1 (bases 1 to 1473)
 AUTHORS McCorquodale, P. and Busch, A.
 TITLE Dye transfer inhibiting compositions
 JOURNAL Patent: EP 0540784-A 3 12-MAY-1993;
 THE PROCTER & GAMBLE COMPANY

FEATURES
 source
 1. 1473
 Location/Qualifiers
 /organism="Fusarium oxysporum"
 /db_xref="taxon:5507"
 97..1227
 /codon_start=1
 /product="endoglucanase"
 /protein_id="CAA0169.1"
 /db_xref="GI:832901"

CDS

1/translacion="MRSYTLALAGPLAVSAAGSGHSTRYWDCCKFCGSGKAAVN
 APLATCDKNDNISNTNAVNGCEGGSAYACTNYSFPAVNDLAVGAATKISGSEA
 BWCACVATLTPTTGGPVKGMKMTVOSTNGDGLDNHEDLAMPFGGAGVIGPCCTSEFG
 ALGAGVIGISRSRSECDVSPILLKDCGMRPDMFNANPDFTFEOVQCPALDLSG
 CKRDDSSFPARKVDLSAKPQSSSAKTTSAALAAPOKTKDSAPVVOKSSKTPPA
 OPEPTPADKPDIDKVPATKPAIKPVOPVAKPKTKTKRGSCPAKTATATA
 SVVPAYVOCGSGSAVPNGNLACATGSKCKVKNERYISQVFN"

BASE COUNT 343 a 453 c 337 g 340 t
 ORIGIN

Query Match 20.1%; Score 218.2; DB 6; Length 1473;
 Best Local Similarity 63.0%; Pred. No. 1e-48;
 Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

QY 449 GTGTGCTCCGGTAATGTTGAACCACTGCTACTGAGATTGTTGAAGCTTTTGCA 508
 DB 143 GTGCTGCTTCTGGAAGCGGTCACTGATGATGCGGATGCTCAAGCCTTCTTGCT 202
 QY 509 GTTGCCCGGTAGGCTGATGTCACCTCCCTGTTGGCTCCCTTAACAAGATGTAAGA 568
 DB 203 CTTGGAAGCGAAGGCTGCTGTCAACGCCCTGCTTTAACTTGTGATTAAGAACGTAACC 262
 QY 569 CTCTTGTGATTAACAACACTCAAAACGCTGT---GTTGTGTAGAGAGCTACACTGTA 625
 DB 263 CCAATTTCACAACAACATGCTGTCAACGTTGTAGAGGTGTGTTGCTTATAGTTGCA 322
 QY 626 ATGACATCAACCTTGGGTTGTTAGCGAGCACTTGGCTTACGTTTCCGCGCTTCCA 685
 DB 323 CCAACTACTCTCTCGGCTGTCAACGATGAGCTTGGCTTACGCTTGTGCTCAACA 382

QY 686 TTTCTGTGTAGAGAGCTACTTGTGTGTGCTGTTTCAACTCAACTCAACTCA 745
 DB 383 TCTCCGGTGTCTCCAGAGCCAGCTGTGCTGTGTGCTTGTGATGTTTACCTTACACTG 442
 QY 746 CTGCGCTCAAGGATTAAGATGTTGTTTCAAGTAACAACACTGTTTCACTTGGCT 805
 DB 443 GCCCGGTCAAGGGCAAGATGATTCGTCAGTCACCAACACTGAGGATCTCGGCG 502
 QY 806 CTACACTGTGTGCTCACTTGTGCAATGCTCCGCTGTGTGTGTTGATATCAAGT 865
 DB 503 AACAC-----CACTTCATCTCATGATGCCGCGGTGTGTGTGTGTGTGACG 553
 QY 866 GTTGTGCACTCAATGGGTGTGCTCCAGATGTTGGGATGCAAGATACGGCGGTGTT 925
 DB 554 GCTGCACTCTGATGTCG-----CAAGCTCTGGGGGCGCCAGTACGGCGGTATCT 607
 QY 926 CTCTGCTGCTGATGTTTAACTCTTCTTCTGCTTCTTCAAGCTGTTGTAAGGAGAT 985
 DB 608 CTTCCGGAAGCGAATGTGATGATACCTCCGAGCTTCTCAAGAGCGTTGCCACTGGGAT 667
 QY 986 TCGGCTGTTCAAAACGCTGATTAACCAACATGACCTACAAACAGTTACTGTCCA 1045
 DB 668 TCGACTGTTGCAAGCGCGACACCTGATCTTCACTTTAGCAGGTTCAGTGGCCCA 727
 QY 1046 AGGCTATCACTGCCAAGTCTGCTG 1070
 DB 728 AGGCTCTCTCGACATCAGTGATG 752

RESULT 9
 A41660 1473 bp DNA linear PAT 05-MAR-1997
 LOCUS Sequence 3 from Patent EP0633311.
 DEFINITION A41660
 ACCESSION A41660 GI:2297285
 VERSION A41660.1 GI:2297285
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 unclassified.

REFERENCE 1 (bases 1 to 1473)
 AUTHORS Herboles, I. M. and Jensen, M. P.
 TITLE Hydrophobic amines for cellulase stabilizant in liquid detergent
 JOURNAL compositions containing anionic surfactant and cellulase
 Patent: EP 0633311-A 3 11-JAN-1995;
 PROCTER & GAMBLE (US)
 Other publication CA 2165771 950105.

FEATURES
 source
 1. 1473
 Location/Qualifiers
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 343 a 453 c 337 g 340 t
 ORIGIN

Query Match 20.1%; Score 218.2; DB 6; Length 1473;
 Best Local Similarity 63.0%; Pred. No. 1e-48;
 Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

QY 449 GTGTGCTCCGGTAATGTTGAACCACTGCTACTGAGATTGTTGAAGCTTTTGCA 508
 DB 143 GTGCTGCTTCTGGAAGCGGTCACTGATGATGCGGATGCTCAAGCCTTCTTGCT 202
 QY 509 GTTGCCCGGTAGGCTGATGTCACCTCCCTGTTGGCTCCCTTAACAAGATGTAAGA 568
 DB 203 CTTGGAAGCGAAGGCTGCTGTCAACGCCCTGCTTTAACTTGTGATTAAGAACGTAACC 262
 QY 569 CTCTTGTGATTAACAACACTCAAAACGCTGT---GTTGTGTAGAGAGCTACACTGTA 625
 DB 263 CCAATTTCACAACAACATGCTGTCAACGTTGTAGAGGTGTGTTGCTTATAGTTGCA 322
 QY 626 ATGACATCAACCTTGGGTTGTTAGCGAGCACTTGGCTTACGTTTCCGCGCTTCCA 685
 DB 323 CCAACTACTCTCTCGGCTGTCAACGATGAGCTTGGCTTACGCTTGTGCTCAACA 382

Oy	686	TTTCGGGAGTGAAGCAACCTCTCTGGTGTGGCCCTGTTGAACTACATTCACCTCTA	745
Db	383	TCTCCGGTGGCTCCGAGGCCAGCTGCTGTGCTGCTTGTATGCTTACCTTCACCACTG	442
Oy	746	CTGCCGTCAAGGGTAAGAGATGGTGTGTTCAAGTAACCAACACTGGTCTGACCTTGACT	805
Db	443	GCCCCGTCAAGGGCAAGAAAGATGATGATCGTCCAGTCCACCAACACTGGAGATGATCTCGGCG	502
Oy	806	CTAACACTGGTGCTCATTCTTTGACTTTGCAAAATGCCGGTGGTGTGTGTATCTACAATG	865
Db	503	ACAAC-----CACTTCGATCTCAATGATGCCCCGGGGGTGTGTGTGTCTTCGACG	553
Oy	866	GTTGGCCACTCAATGGGGGTGCTCCACCGAGTGGTGGGGTCAAGATACGGCGGTGTT	925
Db	554	GCTGCACCTCTGATGTTGCG-----CAAGGCTCTGCGCGGTGACCAGTACGGCGGTATCT	607
Oy	926	CTTTCGCTCTGACTGTTCTACCTTCCTCTGCCCCCTTCAAGCTGGTGTGAATGGAGAT	985
Db	608	CCTCCCGAAGGAATGTATGATACCTCCCGAGCTTCTCAAGAGAGGTTGCCACTGGCGAT	667
Oy	986	TGCGCTGGTTCAAAAGCGCTGATTAACCCACATGATCACTACAAACAGTTACCTGTCCCA	1045
Db	668	TGAGCTGGTTCGAGAGACCCGCAACCTGTACTTACCTTTGAGAGAGGTTCAAGTGCCCCA	727
Oy	1046	AGGCTATCACTGCCAAGTCTGGGCTG	1070
Db	728	AGGCTCTCTCGACATCAAGTGATG	752

[illegible]

Qy	746	CTGCAGCAAGGATGAAGATGGTTGTTCAAGTAAACAACACATGCTTCAACCTTGCT	805
Db	443	GCCCCGTCAAGGGCAAGATGATCGTCCAGTCCACCAACATCTGGAGGTATCTCGGCG	502
Qy	806	CTAACACTGAGTCTCATCTTTGACCTTGCAAAATGCCGGGTGGTGGTGTGTTATTAATATG	865
Db	503	ACAAC-----CACTTCGATCTCATGAATGCCCGGGGGTGGTGTGCGTATCTTCACG	553
Qy	866	GTTGTGCACTCAATAGGGGTGCTCCACCGATGGTGGGGTGCAAGATACGGCGGTGTT	925
Db	554	GCTGCACTCTGAGTGG-----CAAGGCTCTCGGGGGTCCAGTACGGCGGTATCT	607
Qy	926	CTTCTGCTCTGACATGTTCTTAAACCTTCCTTGTGCCCTTCAGCGTGTGTAAAGTGAAT	985
Db	608	CTTCCCGAAGCGAATGTGATAGTACACCCCGAGCTTCTTCAGACGGTGTGCCACTGGCGAT	667
Qy	986	TCGGCTGTTCAAAAACGCTGATTAACCCMACCATGACCTTACAAAACMAATTACTGTGCCA	1045
Db	668	TCGACTGGTTGCAAAACGCCGCAACAACCTTGACTTCACTTGGACAGAGTTCAGTGCCCA	727
Qy	1046	AGGCTATCACTGCCAAGTCTGGCG	1070
Db	728	AGGCTCTCTCGACATCACTGAGATG	752

[illegible]

Db 203 CTGTGGAGGGAAAGGCTGTGTCAAAGCCGCTCTTAACTTGGATTAAGAAAGAAAC 262

Qy 569 CTCCTTGGATTAACAACACTGAAAAGCGCTGT---GTGGGTGGATAGAGCTAACCTGTGA 625

Db 263 CCATTTCCAAACCAATGCTGTCAACGGTGTGTAGAGGTGTGTGTCTGTCTTAAGCTTSCA 322

Qy 626 ATGACATCAACCTTGGGTGTGTAGCGACGACCTTGCCTAGCGTTTGGCCGTGTCTCA 685

Db 323 CCACATATCTCTCCTGTGGGTGTGTCAACGATAGCTTCTGTACGGTTTGGCTGTACACAGA 382

Qy 686 TTTCTGTGTGTAGCGAAGCTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 745

Db 383 TCTCCGGTGGGTCCGAGGCGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 442

Qy 746 CTGCGGTAAAGGGTAAGAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 805

Db 443 GCCCGGTCAAGGGGAAGAAAGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 502

Qy 806 CTAAACACTGTGTGTCTACTTGTGCTTGCAGAAATGCGCGGTGTGTGTGTGTGTGTGTGTGTGT 865

Db 503 ACAAAC-----CACTTGTGATCTCATGATGATCCCGCGGTGTGTGTGTGTGTGTGTGTGTGT 553

Qy 866 GTTGTGCACACTCATGTGGGT 925

Db 554 GCTGTGACCTGTGAGTTTCGG-----CAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 607

Qy 926 CTTTGTGCTCTGTACTGTGTCTTAACTTCTTCTGTGCGCTTCAAGCTGTGTGTGTGTGTGTGT 985

Db 608 CCTCCCGAAGCGATGT 667

Qy 986 TCGGCTGT 1045

Db 668 TGTGATGT 727

Qy 1046 AAGCTTATATCTGTCAAGTCTGTGCTGT 1070

Db 728 AAGCTTCTCTGTGATCATCAAGTGTGT 752

RESULT 12	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BD010853	BD010853	Cellulase preparation containing endoglucanase.	BD010853	1	GI:18639226	JP 2001057894-A/2.						
						JP 2001057894-A/2.						
						Fusarium oxysporum						
						Fusarium oxysporum						
						Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.						
						1 (bases 1 to 1473)						
						Rasmussen,G., Mikkelsen,J.M., Schilein,M., Packar,S.A., Hagen,F., Miland,H.K. and Halstrop,S.						
						Cellulase preparation containing endoglucanase						
						Patent: JP 2001057894-A 2 06-MAR-2001;						
						NOVO NORDISK AS						
						OS Fusarium oxysporum						
						PN JP 2001057894-A/2						
						PD 06-MAR-2001						
						PF 06-JUL-2000 JP 2000205757						
						PR 09-MAY-1990 DK 1159/90, 22-APR-1991 DK 0736/91 PI						
						GURETH RASMUSSEN, JAN MOLLER MIKKELSEN, MARTIN SCHILEIN, PI						
						SHAKUNT ANANT PATKAR, FRED HAGEN, HJORT KARSTEN MILAND, PI						
						HALSTROP						
						PC C12N15/09 C11D3/386 C12N1/15 C12N1/19 C12N9/24 D06G16/00// FC						
						(C12N15/09, C12R1/77), (C12N15/09, C12R1/645), (C12N9/24, FC						
						C12R1/685), (C12N9/24, C12R1/885), (C12N9/24, C12R1/78), (C12N9/24, C12R1/65),						
						PC (C12N9/24, C12R1/685), C12N15/00, C12N15/77),						
						(C12N15/00, FC C12R1/645)						
						CC						
						FN Key /						
						Location/Qualifiers						

FEATURES	FT	CDS	97	.1224	
source		Location/Qualifiers			
		1..1473			
		/organism="Fusarium oxysporum"			
		/db_xref="cazon:5507"			
BASE COUNT	343	a	453	c	337
ORIGIN		g		340	t

```

Query Match Score 20.1%; Score 218.2; DB 6; Length 1473;
Best Local Similarity 63.0%; Pred. No. 1e-48;
Matches 334; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

OY GTGTGGCTCCGGTAATGTGTAAACATCTCGACTGGGATTTGTGTAAAGCTTTGTGA 508
Db 143 GGTCTGCTTTGAAAGCGTCACTCTATCTGATCTGGGATTTCTGAAACCTTTTGT 202
OY 509 GTTGCCCGGTAAAGCTGATATGCTCTCCCTCTTGGCTCTCTTAAACAAAGATGTGA 568
Db 203 GTTGAGAGGAAAGGTGTGTGTCAAGCCCTCTCTTAACTTGATTAAGAAAGACAAAC 262
OY 569 CTCTTGCTGATTAACAACATCACTAAAGCGTGT--GTTGGTGTAGACGCTACCTGTA 625
Db 263 CCAATTTCAACAACAATGTGTCAACGGTGTGTAGGGGTGTGTCTTGTCTTAATGTGA 322
OY 626 ATGCAATCAACCTTGTTGGTGTATGACACACCTTGCCTACGATTTGCGCGTCTTCA 685
Db 323 CCAACTCTCTCCCTGGGTGTCAACGATGATGATTCCTACGATTTGCGCTTACCAAG 382
OY 686 TTTCGAGGTATACGAAGCTACTTGAGTGTGTGTCCTGTTTGAACACTCAATCACTTA 745
Db 383 TCTCGGAGCTCCAGGACAGCTGTGTGTCTTGCTTAAGTTTGAACCTTCAACACTG 442
OY 746 CTGCGCTCAAGGTAAGAAAGATGGTGTAAAGTAACCAACAACATGTTTGAACCTTGCT 805
Db 443 GCCCGTAAAGGCAAGAAAGATGATCGTCAAGTCAACAACATCTGAGAGTGACTCGGG 502
OY 806 CTAAACAGTGTCTCACTTTGACTTGCAAAATGCCGGTGTGTGTGTGTGTATCTAATG 865
Db 503 ACAA-----CACTTCATCTCATATGATCCGCGGTGTGTGTGTGTATCTTGAGC 553
OY 866 GTTGTGCACCTCAATGGGTGTCTCCACCGATGGTGTGGGTGCAAGATACGCGGTGT 925
Db 554 GGTGACCTCTGAGTTCCG-----CAAGGCTCTCGCGGTGTCCAGTAAAGGGGATATC 607
OY 926 CTTCGCTCTGACTGTTTAACTTCTCTCTGCTCCCTTGAAGCTGTGTAAATGAGAT 985
Db 608 CTTCCCAAGGATGTATTACTTAACCCGAGCTTCTCAAGGACGGTTGCCATCTGCGAT 667
OY 986 TCGGCTGTCAAAAAGCTGTAAACCAACATATGACTTAAACAACAGTATACCTGTCCA 1045
Db 668 TGAAGTGTGAAAGACGCGCAAACTCTTAACCTTTAGAGAGTTCAATGCGCCA 727
OY 1046 AAGCTATCACTGCGCAATGTGGCTG 1070
Db 728 AAGCTCTCTGACATCAATGGAATG 752

```

RESULT 13				
LOCUS	113885	1473 bp	DNA	linear
DEFINITION	Sequence 3 from patent US 5443750.			
ACCESSION	113885			
VERSION	113885.1	GI:996365		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1473)			
AUTHORS	Convents A., Busch, A. and Baeck, A.C.			
TITLE	Detergent compositions with high activity cellulase and softening			
JOURNAL	Patent: US 5443750-A 3 22-AUG-1995;			
FEATURES	Location/Qualifiers			

source 1.1473
/organism="unknown"
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 20.1%; Score 218.2; DB 6; Length 1473;
Best Local Similarity 63.0%; Pred. No. 1e-48;
Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

449 GTGTCCTCCGTAATGTAAGTAACCACTGCTACTGGAATGTTGTAAGCTTCTTGA 508
143 GTGTCCTCCGTAAGGAGGCTACTCTACTGATCTGGAATGCTGCAAGCTTCTTGT 202
509 GTTGCCCGGTAAGGCTGATGTAACCTCCCTGTTGGCTCCCTGTAACAAGATGTAAGA 568
203 CTGGAAGGAAAGGCTGCTGTAACGCGCTTTAACTTGTGATGAAGAACACCAACC 262
569 CTCTTGCTGATTAACAACCTCAAAACGGCTGT---GTTGTGTGAGCAGCTACCTGTA 625
263 CCAATTCACACCAACATGCTGTCAACGGTTGAGGGGTGTGCTTATGCTTGA 322
626 ATGACATCAACCTTGGTGTGACGACGACTTGGCTTACGCTTGGCGCTGCTTCA 685
323 CCAACTACTCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGCTTCCCTACCAAGA 382
686 TTTCTGCTGAGGAGGCTACTTGGTGTGCTGCTGTTGGAAGCTCACTTCACTTCA 745
383 TCTCCGGTGTCCGAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 442
746 CTGCGCTCAAGGCTAAGATGATGTTGTAAGTAACAACCACTGTTCTGACCTTGGCT 805
443 GCCCGTCAAGGCTAAGATGATGTTGTAAGTAACAACCACTGTTCTGACCTTGGCT 502
806 CTAACTGCTGCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 865
503 ACAAC-----CACTTGATCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
866 GTTGTCCTCACTCAATGAGGCTGCTCCACGATGTTGAGGCTGCAAGATGAGGCTGTT 925
554 GCTGCACTCTGATGTTGG-----CAAGGCTCTGCGGCTGCTGCTGCTGCTGCTGCT 607
926 CTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 985
608 CTTCCCGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
986 TCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1045
668 TCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
QY 1046 AGGCTATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070
Db 728 AGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752

RESULT 14
121317 1473 bp DNA linear PAT 07-OCT-1996
LOCUS
DEFINITION Sequence 3 from patent US 5520838.
ACCESSION 121317
VERSION 121317.1 GI:1601671
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1473)
AUTHORS Baack, A.C., Ceulemans, R.A. and Busch, A.
TITLE Compact detergent compositions with high activity cellulase
JOURNAL Patent: US 5520838-A 3 28-MAY-1996;
FEATURES
Location/Qualifiers
1.1473
source

BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 20.1%; Score 218.2; DB 6; Length 1473;
Best Local Similarity 63.0%; Pred. No. 1e-48;
Matches 394; Conservative 0; Mismatches 213; Indels 18; Gaps 3;

449 GTGTCCTCCGTAATGTAAGTAACCACTGCTACTGGAATGTTGTAAGCTTCTTGA 508
143 GTGTCCTCCGTAAGGAGGCTACTCTACTGATCTGGAATGCTGCAAGCTTCTTGT 202
509 GTTGCCCGGTAAGGCTGATGTAACCTCCCTGTTGGCTCCCTGTAACAAGATGTAAGA 568
203 CTGGAAGGAAAGGCTGCTGTAACGCGCTTTAACTTGTGATGAAGAACACCAACC 262
569 CTCTTGCTGATTAACAACCTCAAAACGGCTGT---GTTGTGTGAGCAGCTACCTGTA 625
263 CCAATTCACACCAACATGCTGTCAACGGTTGAGGGGTGTGCTTATGCTTGA 322
626 ATGACATCAACCTTGGTGTGACGACGACTTGGCTTACGCTTGGCGCTGCTTCA 685
323 CCAACTACTCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGCTTCCCTACCAAGA 382
686 TTTCTGCTGAGGAGGCTACTTGGTGTGCTGCTGTTGGAAGCTCACTTCACTTCA 745
383 TCTCCGGTGTCCGAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 442
746 CTGCGCTCAAGGCTAAGATGATGTTGTAAGTAACAACCACTGTTCTGACCTTGGCT 805
443 GCCCGTCAAGGCTAAGATGATGTTGTAAGTAACAACCACTGTTCTGACCTTGGCT 502
806 CTAACTGCTGCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 865
503 ACAAC-----CACTTGATCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
866 GTTGTCCTCACTCAATGAGGCTGCTCCACGATGTTGAGGCTGCAAGATGAGGCTGTT 925
554 GCTGCACTCTGATGTTGG-----CAAGGCTCTGCGGCTGCTGCTGCTGCTGCTGCT 607
926 CTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 985
608 CTTCCCGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
986 TCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1045
668 TCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
QY 1046 AGGCTATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070
Db 728 AGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752

RESULT 15
157984 1473 bp DNA linear PAT 07-OCT-1997
LOCUS
DEFINITION Sequence 3 from patent US 5610129.
ACCESSION 157984
VERSION 157984.1 GI:2483048
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1473)
AUTHORS McCorquodale, F. and Busch, A.
TITLE Dye transfer inhibiting compositions
JOURNAL Patent: US 5610129-A 3 11-MAR-1997;
FEATURES
Location/Qualifiers
1.1473
source

BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

```
OY 449 GTGGTCCCTCCGTAATGATGAAACACTGCTACTGGGATTTGTTGAACCTCTTGTCA 508
DB 143 GTGCTGCTCTTGGAAGCCGTCACCTCTACGATATCGGATTTGTCGAAGCCTCTTGTCT 202
OY 509 GTTGCCCGGTAAAGCTGATGTCACTCCCTGTGTGAGTCTGTAAACAAGATGATAGA 568
DB 203 CTTGAGCGGAAGGCTGCTGTCAACGCCCTGCTTAACTTGATTAAGAAACAACACC 262
OY 569 CTCTGTGATTAACAACAACCTCAAAACGAGCTGT---GTTGGTGTAGCAAGCTACAACCTGTA 625
DB 263 CCATTTCACAACAACATGCTGTCAACGATGTGTAGAGGTGTGTCTGTATGTGTCA 322
OY 626 ATGACAATCAACCTTGGGTTGTTAAGCAACGACTTGCTACGATTTCCGCGCTTCCA 685
DB 323 CCAACTACTCTCCCTGGGCTGTCAACGATGAGCTTACGATTCGCTGTACCAAGA 382
OY 686 TTTCTGTGTAGCGAAGCTACTGTGTGTGTGCTGTTCGAACTCAATTCACCTCTA 745
DB 383 TCTCCGATGCTCCGAGGCGAGCTGTGTGTGTGTGTATGTGTGACCTTCAACCACTG 442
OY 746 CTGCGGTCAAGGTAAGAAGATGTTGTCAAGTAAACAACAACCTGATCTGACCTTGGCT 805
DB 443 GCGCCGTCAAGGCAAGATGATGATCTTCCAGTCCACAACAACCTGAGGTGATCTCGCG 502
OY 806 CTAACTGTGTGTCTACTTTGACTTGTCAATGCCGCTGTGTGTGTGTGTGTATCTAACATG 865
DB 503 ACAAC-----CACTTCATCTCATGATGCCGCGGTGTGTGTGTGTGTGTGTGTGTGTG 553
OY 866 GTTGTCCACTCAATGGGCTGTCTCCACCAACGATGATGAGGTGTGCAAGATACGCGGTGTT 925
DB 554 GCTGCACTCTGTGATTCGG-----CAAGGCTCTCGCGGTGTGCCAGTACGCGGTATCT 607
OY 926 CTCTGCTCTGTGACTTCTTAACCTTCTTGTGCTTCAAGCTGTGTGTGTGTGTGTGTGTGT 985
DB 608 CTTCCGGAAGCGATGTGTATGATTAAGTACCCGAGCTTCTCAAGAGCGTTGTGCCACTGGGAT 667
OY 986 TCGGCTGTGTCAAAAACGTGTATTAACCAACATGACTTACAAACAAGTACTGTGCCA 1045
DB 668 TCGACTGTGTGTGGAAGCGCGACAACCTGACTTCACTTGTGAGAGGTTCAGTGTGCCA 727
OY 1046 AGGCTATCACTGCAAGTGTGCTG 1070
DB 728 AGGCTCTCTCGACATCAAGTGTGATG 752
```

Search completed: June 17, 2003, 16:24:49
Job time : 2791.18 secs